

1 GCTACGCGGGCCACGCTGCTGGCTGGCCTGACCTAGGCGCGCGGGGTGCGGCGGCCGCGCGGGCGGGCT  
70 GAGTGAGCAAGACAAGACACTCAAGAAGAGCGAGCTGCGCCTGGGTCCCGGCCAGGCTTGACGCGAGAG  
139 GCGGCGGGCAGACGGTGCCCGGCGGAATCTCTGAGCTCCGCGGCCAGCTCTGGTGCCAGCGCCAGT  
208 GGCGCGCGCTTCGAAAGTGAAGTGGTGCCTCGCGCCCTCTCTCGGTGCGGGACCATGAAGCTGCTGCCG  
M K L L P  
1  
277 TCGGTGGTGTCTGAAGCTCTTTCTGGCTGCAGTTCTCTCGGCACCTGGTGACTGGCGAGAGCCTGGAGCGG  
S V V L K L F L A A V L S A L V T G E S L E R  
10 20  
346 CTTCGAGAGGGCTAGCTGCTGGAACCAAGCAACCCGACCCCTCCCACTGTATCCACGGACCAAGCTGCTA  
L R R G L A A G T S N P D P P T V S T D Q L L  
30 40 50  
415 CCCCTAGGAGGCGGCGGGGACCGGAAAGTCCCTGACTTGCAAGAGGCAGATCTGGACCTTTTGAGAGTC  
P L G G G R D R K V R D L Q E A D L D L L R V  
60 70  
484 ACTTTATCCTCCAAGCCACAAGCACTGGCCACACCAACAAGGAGGAGCACGGGAAAAGAAAGAGAAA  
T L S S K P Q A L A T P N K E E H G K R K K K  
80 90  
553 GGCAAGGGGCTAGGGAAGAAGAGGGACCCATGTCTTCGGAAATACAAGGACTTCTGCATCCATGGAGAA  
G K G L G K K R D P C L R K Y K D F C I B G E  
100 110 120  
622 TGCAAAATATGTGAAGGAGCTCCGGGCTCCCTCCTGCATCTGCCACCCGGGTTACCATGGAGAGAGGTGT  
C K Y V R E L R A P S C I C H P G Y H G E R C  
130 140  
691 CATGGGCTGAGCCTCCAGTGGAATAATCGCTTATATACCTATGACCACACAACCATCCTGGCCGTGGTG  
H G L S L P V E N R L Y T Y D E T T I L A V V  
150 160  
760 GCTGTGGTGTCTGTCATCTGTCTGTCTGCTGGTTCATCGTGGGGCTTCTCATGTTTAGGTACCATAGGAGA  
A V V L S S V C L L V I V G L L M F R Y H R R  
170 180  
829 GGAGGTTATGATGTGGAATAATGAAGAGAAAGTGAAGTTGGGCATGACTAATTCCTCACTGA (SER ID NO:1)  
G G Y D V E N E E K V K L G M T N S E (SER ID NO:2)  
190 200

Fig. 1